

OIEP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/993,180

DATE: 12/05/2001

TIME: 11:53:53

Input Set : A:\es.txt

Output Set: N:\CRF3\11212001\I993180.raw

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3 <110> APPLICANT: Bristol-Myers Squibb Company
5 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN SERPIN SECRETED FROM
LYMPHOID
6     CELLS, LSI-01
8 <130> FILE REFERENCE: D0051.NP
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/993,180
C--> 10 <141> CURRENT FILING DATE: 2001-11-14
10 <150> PRIOR APPLICATION NUMBER: US 60/248,434
11 <151> PRIOR FILING DATE: 2000-11-14
13 <150> PRIOR APPLICATION NUMBER: US 60/257,610
14 <151> PRIOR FILING DATE: 2000-12-21
16 <150> PRIOR APPLICATION NUMBER: US 60/282,745
17 <151> PRIOR FILING DATE: 2001-04-10
19 <160> NUMBER OF SEQ ID NOS: 46
21 <170> SOFTWARE: PatentIn version 3.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1766
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (68)..(1372)
32 <400> SEQUENCE: 1
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35 accaacc atg caa gga cag ggc agg aga aga gga acc tgc aaa gac ata      109
36     Met Gln Gly Gln Gly Arg Arg Arg Gly Thr Cys Lys Asp Ile
37     1             5             10
39 ttt tgt tcc aaa atg gca tct tac ctt tat gga gta ctc ttt gct gtt      157
40 Phe Cys Ser Lys Met Ala Ser Tyr Leu Tyr Gly Val Leu Phe Ala Val
41 15             20             25             30
43 ggc ctc tgt gct cca atc tac tgt gtg tcc ccg gcc aat gcc ccc agt      205
44 Gly Leu Cys Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser
45             35             40             45
47 gca tac ccc cgc cct tcc tcc aca aag agc acc cct gcc tca cag gtg      253
48 Ala Tyr Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val
49             50             55             60
51 tat tcc ctc aac acc gac ttt gcc ttc cgc cta tac cgc agg ctg gtt      301
52 Tyr Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val
53             65             70             75
55 ttg gag acc ccg agt cag aac atc ttc ttc tcc cct gtg agt gtc tcc      349
56 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val Ser
57             80             85             90
59 act tcc ctg gcc atg ctc tcc ctt ggg gcc cac tca gtc acc aag acc      397
60 Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr Lys Thr
61 95             100             105             110
63 cag att ctc cag ggc ctg ggc ttc aac ctc aca cac aca cca gag tct      445
64 Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr Pro Glu Ser
65             115             120             125

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67	gcc atc cac cag ggc ttc cag cac ctg gtt cac tca ctg act gtt ccc	493
68	Ala Ile His Gln Gly Phe Gln His Leu Val His Ser Leu Thr Val Pro	
69	130 135 140	
71	agc aaa gac ctg acc ttg aag atg gga agt gcc ctc ttc gtc aag aag	541
72	Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala Leu Phe Val Lys Lys	
73	145 150 155	
75	gag ctg cag ctg cag gca aat ttc ttg ggc aat gtc aag agg ctg tat	589
76	Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly Asn Val Lys Arg Leu Tyr	
77	160 165 170	
79	gaa gca gaa gtc ttt tct aca gat ttc tcc aac ccc tcc att gcc cag	637
80	Glu Ala Glu Val Phe Ser Thr Asp Phe Ser Asn Pro Ser Ile Ala Gln	
81	175 180 185 190	
83	gcg agg atc aac agc cat gtg aaa aag aag acc caa ggg aag gtt gta	685
84	Ala Arg Ile Asn Ser His Val Lys Lys Lys Thr Gln Gly Lys Val Val	
85	195 200 205	
87	gac ata atc caa ggc ctt gac ctt ctg acg gcc atg gtt ctg gtg aat	733
88	Asp Ile Ile Gln Gly Leu Asp Leu Leu Thr Ala Met Val Leu Val Asn	
89	210 215 220	
91	cac att ttc ttt aaa gcc aag tgg gag aag ccc ttt cac ctt gaa tat	781
92	His Ile Phe Phe Lys Ala Lys Trp Glu Lys Pro Phe His Leu Glu Tyr	
93	225 230 235	
95	aca aga aag aac ttc cca ttc ctg gtg ggc gag cag gtc act gtg caa	829
96	Thr Arg Lys Asn Phe Pro Phe Leu Val Gly Glu Gln Val Thr Val Gln	
97	240 245 250	
99	gtc ccc atg atg cac cag aaa gag cag ttc gct ttt ggg gtg gat aca	877
100	Val Pro Met Met His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr	
101	255 260 265 270	
103	gag ctg aac tgc ttt gtg ctg cag atg gat tac aag gga gat gcc gtg	925
104	Glu Leu Asn Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val	
105	275 280 285	
107	gcc ttc ttt gtc ctc cct agc aag ggc aag atg agg caa ctg gaa cag	973
108	Ala Phe Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln	
109	290 295 300	
111	gcc ttg tca gcc aga aca ctg ata aag tgg agc cac tca ctc cag aaa	1021
112	Ala Leu Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys	
113	305 310 315	
115	agg tgg ata gag gtg ttc atc ccc aga ttt tcc att tct gcc tcc tac	1069
116	Arg Trp Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser Tyr	
117	320 325 330	
119	aat ctg gaa acc atc ctc ccg aag atg ggc atc caa aat gcc ttt gac	1117
120	Asn Leu Glu Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala Phe Asp	
121	335 340 345 350	
123	aaa aat gct gat ttt tct gga att gca aag aga gac tcc ctg cag gtt	1165
124	Lys Asn Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser Leu Gln Val	
125	355 360 365	
127	tct aaa gca acc cac aag gct gtg ctg gat gtc agt gaa gag ggc act	1213
128	Ser Lys Ala Thr His Lys Ala Val Leu Asp Val Ser Glu Glu Gly Thr	
129	370 375 380	
131	gag gcc aca gca gct acc acc acc aag ttc ata gtc cga tcg aag gat	1261

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132 Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile Val Arg Ser Lys Asp
133           385                      390                      395
135 ggt ccc tct tac ttc act gtc tcc ttc aat agg acc ttc ctg atg atg      1309
136 Gly Pro Ser Tyr Phe Thr Val Ser Phe Asn Arg Thr Phe Leu Met Met
137       400                      405                      410
139 att aca aat aaa gcc aca gac ggt att ctc ttt cta ggg aaa gtg gaa      1357
140 Ile Thr Asn Lys Ala Thr Asp Gly Ile Leu Phe Leu Gly Lys Val Glu
141 415                      420                      425                      430
143 aat ccc act aaa tcc taggtgggaa atggcctggt aactgatggc acattgctaa      1412
144 Asn Pro Thr Lys Ser
145           435
147 tgcacaagaa ataacaaacc acatccctct ttctgtttctg aggggtgcatt tgacccccagt      1472
149 ggagctggat tcgctggcag ggatgccact tccaaggctc aatcaccaaa ccatcaacag      1532
151 ggacccccagt cacaagccaa caccatttaa cccagtcag tgcccttttc cacaaattct      1592
153 cccaggtaac tagcttcatt ggatgttgct gggttaccat atttccattc cttggggctc      1652
155 ccaggaatgg aaatacgcca acccagggtta ggcacctcta ttgcagaatt acaataacac      1712
157 attcaataaaa actaaaatat gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa      1766
160 <210> SEQ ID NO: 2
161 <211> LENGTH: 435
162 <212> TYPE: PRT
163 <213> ORGANISM: Homo sapiens
165 <400> SEQUENCE: 2
167 Met Gln Gly Gln Gly Arg Arg Arg Gly Thr Cys Lys Asp Ile Phe Cys
168 1           5           10           15
171 Ser Lys Met Ala Ser Tyr Leu Tyr Gly Val Leu Phe Ala Val Gly Leu
172       20           25           30
175 Cys Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr
176       35           40           45
179 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr Ser
180       50           55           60
183 Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val Leu Glu
184 65           70           75           80
187 Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val Ser Thr Ser
188       85           90           95
191 Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr Lys Thr Gln Ile
192       100          105          110
195 Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr Pro Glu Ser Ala Ile
196       115          120          125
199 His Gln Gly Phe Gln His Leu Val His Ser Leu Thr Val Pro Ser Lys
200       130          135          140
203 Asp Leu Thr Leu Lys Met Gly Ser Ala Leu Phe Val Lys Lys Glu Leu
204 145          150          155          160
207 Gln Leu Gln Ala Asn Phe Leu Gly Asn Val Lys Arg Leu Tyr Glu Ala
208       165          170          175
211 Glu Val Phe Ser Thr Asp Phe Ser Asn Pro Ser Ile Ala Gln Ala Arg
212       180          185          190
215 Ile Asn Ser His Val Lys Lys Lys Thr Gln Gly Lys Val Val Asp Ile
216       195          200          205
219 Ile Gln Gly Leu Asp Leu Leu Thr Ala Met Val Leu Val Asn His Ile

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220      210      215      220
223 Phe Phe Lys Ala Lys Trp Glu Lys Pro Phe His Leu Glu Tyr Thr Arg
224 225      230      235      240
227 Lys Asn Phe Pro Phe Leu Val Gly Glu Gln Val Thr Val Gln Val Pro
228      245      250      255
231 Met Met His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr Glu Leu
232      260      265      270
235 Asn Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe
236      275      280      285
239 Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala Leu
240      290      295      300
243 Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys Arg Trp
244 305      310      315      320
247 Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser Tyr Asn Leu
248      325      330      335
251 Glu Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala Phe Asp Lys Asn
252      340      345      350
255 Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser Leu Gln Val Ser Lys
256      355      360      365
259 Ala Thr His Lys Ala Val Leu Asp Val Ser Glu Glu Gly Thr Glu Ala
260      370      375      380
263 Thr Ala Ala Thr Thr Thr Lys Phe Ile Val Arg Ser Lys Asp Gly Pro
264 385      390      395      400
267 Ser Tyr Phe Thr Val Ser Phe Asn Arg Thr Phe Leu Met Met Ile Thr
268      405      410      415
271 Asn Lys Ala Thr Asp Gly Ile Leu Phe Leu Gly Lys Val Glu Asn Pro
272      420      425      430
275 Thr Lys Ser
276      435
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280 <211> LENGTH: 423
281 <212> TYPE: PRT
282 <213> ORGANISM: Homo sapiens
284 <400> SEQUENCE: 3
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287 1      5      10      15
289 Phe Cys Pro Ala Val Leu Cys His Pro Asn Ser Pro Leu Asp Glu Glu
290      20      25      30
292 Asn Leu Thr Gln Glu Asn Gln Asp Arg Gly Thr His Val Asp Leu Gly
293      35      40      45
295 Leu Ala Ser Ala Asn Val Asp Phe Ala Phe Ser Leu Tyr Lys Gln Leu
296      50      55      60
298 Val Leu Lys Ala Pro Asp Lys Asn Val Ile Phe Ser Pro Leu Ser Ile
299 65      70      75      80
301 Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala His Asn Thr Thr Leu
302      85      90      95
304 Thr Glu Ile Leu Lys Gly Leu Lys Phe Asn Leu Thr Glu Thr Ser Glu
305      100      105      110
307 Ala Glu Ile His Gln Ser Phe Gln His Leu Leu Arg Thr Leu Asn Gln

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308          115          120          125
310 Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn Ala Met Phe Val Lys
311          130          135          140
313 Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu Asp Ala Lys Arg Leu
314 145          150          155          160
316 Tyr Gly Ser Glu Ala Phe Ala Thr Asp Phe Gln Asp Ser Ala Ala Ala
317          165          170          175
319 Lys Lys Leu Ile Asn Asp Tyr Val Lys Asn Gly Thr Arg Gly Lys Ile
320          180          185          190
322 Thr Asp Leu Ile Lys Asp Leu Asp Ser Gln Thr Met Met Val Leu Val
323          195          200          205
325 Asn Tyr Ile Phe Phe Lys Ala Lys Trp Glu Met Pro Phe Asp Pro Gln
326          210          215          220
328 Asp Thr His Gln Ser Arg Phe Tyr Leu Ser Lys Lys Lys Trp Val Met
329 225          230          235          240
331 Val Pro Met Met Ser Leu His His Leu Thr Ile Pro Tyr Phe Arg Asp
332          245          250          255
334 Glu Glu Leu Ser Cys Thr Val Val Glu Leu Lys Tyr Thr Gly Asn Ala
335          260          265          270
337 Ser Ala Leu Phe Ile Leu Pro Asp Gln Asp Lys Met Glu Glu Val Glu
338          275          280          285
340 Ala Met Leu Leu Pro Glu Thr Leu Lys Arg Trp Arg Asp Ser Leu Glu
341          290          295          300
343 Phe Arg Glu Ile Gly Glu Leu Tyr Leu Pro Lys Phe Ser Ile Ser Arg
344 305          310          315          320
346 Asp Tyr Asn Leu Asn Asp Ile Leu Leu Gln Leu Gly Ile Glu Glu Ala
347          325          330          335
349 Phe Thr Ser Lys Ala Asp Leu Ser Gly Ile Thr Gly Ala Arg Asn Leu
350          340          345          350
352 Ala Val Ser Gln Val Val His Lys Ala Val Leu Asp Val Phe Glu Glu
353          355          360          365
355 Gly Thr Glu Ala Ser Ala Ala Thr Ala Val Lys Ile Thr Leu Leu Ser
356          370          375          380
358 Ala Leu Val Glu Thr Arg Thr Ile Val Arg Phe Asn Arg Pro Phe Leu
359 385          390          395          400
361 Met Ile Ile Val Pro Thr Asp Thr Gln Asn Ile Phe Phe Met Ser Lys
362          405          410          415
364 Val Thr Asn Pro Lys Gln Ala
365          420
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368 <211> LENGTH: 427
369 <212> TYPE: PRT
370 <213> ORGANISM: Homo sapiens
372 <400> SEQUENCE: 4
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375 1          5          10          15
377 Leu Ser His Gly Gln Leu His Val Glu His Asp Gly Glu Ser Cys Ser
378          20          25          30
380 Asn Ser Ser His Gln Gln Ile Leu Glu Thr Gly Glu Gly Ser Pro Ser

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VERIFICATION SUMMARY

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Input Set : A:\es.txt

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date